a1 cont. herein by reference in their entirety. --

Please replace the paragraph beginning at page 7, line 21, with the following rewritten paragraph. Per 37 C.F.R. §1.121, this paragraph is also shown in Appendix A with notations to indicate the changes made.

a2 -- **Fig. 1.** Nucleotide sequence alignment of wild type *atzA* (bottom sequence) from *Pseudomonas sp.* strain ADP and clone (A7) (SEQ ID NO:1 and SEQ ID NO:3). The boxed sequences indicate areas of nonidentity between the two nucleotide sequences. --

Please replace the paragraph beginning at page 7, line 24, with the following rewritten paragraph. Per 37 C.F.R. §1.121, this paragraph is also shown in Appendix A with notations to indicate the changes made.

a3 -- **Fig. 2.** Nucleotide sequence alignment of wild type *atzA* (bottom sequence) from *Pseudomonas sp.* strain ADP and clone (T7) (SEQ ID NO: 1 and SEQ ID NO:4). The boxed sequences indicate areas of nonidentity between the two nucleotide sequences. --

Please replace the paragraph beginning at page 7, line 27, with the following rewritten paragraph. Per 37 C.F.R. §1.121, this paragraph is also shown in Appendix A with notations to indicate the changes made.

a4 -- **Fig. 3.** Amino acid sequence alignment of wild type AtzA (bottom sequence) from *Pseudomonas sp.* strain ADP and clone (A7) (SEQ ID NO:2 and SEQ ID NO:5). The boxed sequences indicate areas of nonidentity between the two amino acid sequences. Start, indicates beginning of the protein; Stop, indicates end of the protein. --

Please replace the paragraph beginning at page 7, line 30, with the following rewritten paragraph. Per 37 C.F.R. §1.121, this paragraph is also shown in Appendix A with notations to indicate the changes made.

a5 -- **Fig. 4.** Amino acid sequence alignment of wild type AtzA from *Pseudomonas sp.* strain ADP and clone (T7) (SEQ ID NO:2 and SEQ ID NO:6). The boxed sequences indicate areas of nonidentity between the two amino acid sequences. Start, indicates beginning of the protein; Stop, indicates end of the protein. --

Please replace the paragraph beginning at page 8, line 1, with the following rewritten paragraph. Per 37 C.F.R. §1.121, this paragraph is also shown in Appendix A with notations to indicate the changes made.

-- **Fig. 5.** Nucleotide sequence alignment of wild type *atzA* (SEQ ID NO:1, bottom sequence) from *Pseudomonas sp.* strain ADP and clone (A11). Fig. 5(a) provides the sequence from nucleic acids 11-543 (SEQ ID NO:7), Fig. 5(b) provides the sequence from nucleic acids 454-901 (SEQ ID NO:8), Fig. 5(c) provides the sequence from 1458-1851 (SEQ ID NO:9; N in this sequence indicates that this nucleotide has not been verified) and Fig. 5(d) provides the sequence from nucleic acids 1125-1482 (SEQ ID NO:10) of clone A11. The boxed sequences indicate areas of nonidentity between the two nucleotide sequences. The "N" in these sequences refer to nucleic acids that are being verified. The four "C" nucleotides depicted above the top sequence in 5(a) and the eleven "G" nucleotides depicted above the top sequence in 5(b) indicate the correct nucleotide sequence of the top sequence. --

Please replace the paragraph beginning at page 26, line 22, with the following rewritten paragraph. Per 37 C.F.R. §1.121, this paragraph is also shown in Appendix A with notations to indicate the changes made.

-- Recursive sequence recombination was performed by modifications of existing procedures (Stemmer, W., Proc. Natl. Acad. Sci. USA 91:10747-10751 (1994) and Stemmer, W. Nature 370:389-391 (1994)). The entire 8.4 kb plasmid was treated with DNAase I in 50 mM Tris-Cl pH 7.5, 10 mM $MnCl_2$ and fragments between 500 and 2000 bp were gel purified. The fragments were assembled in a PCR reaction using Tth-XL enzyme and buffer from Perkin Elmer, 2.5 mM MgOAc, 400 μM dNTPs and serial dilutions of DNA fragments. The assembly reaction was performed in an MJ Research "DNA Engine" thermocycler programmed with the following cycles:

1	94°C, 20 seconds
2	94°C, 15 seconds
3	40°C, 30 seconds
4	72°C, 30 seconds + 2 seconds per cycle
5	go to step 2 39 more times
6	4°C --